

1 GAACCCAGTT GCTTCAGCGA GTCGAAC TAC AGTTTAACC TCATCAAATA  
51 TGGCATCTCC CTTGCTTGCT GCAGCAGGGA TGGAGAAAT GTCACTTTCT  
101 TTTAACGCTA GCAAGCTTT TCTTTTCTT TTTCTCTTC TATTTAAAAA  
151 TTCTAATCAT GGATGCTTCT TCCGACCTT ATTGCCTTA TGACGGGGGA  
201 GGAGACAATA TTCCCTGAG GGAATTACAT AAAAGAGGAA CTCATTATAC  
251 AATGACAATAA GGAGGCAGCA TTAACAGTTC TACACATTAA CTGGATCTT  
301 TGGATGAACC AATTCCAGGT GTTGGTACAT ATGATGATTT CCATACTATT  
351 GATTGGTGC GAGAAAAATG TAAAGACAGA GAAAGGCATA GACGGATCAA  
401 CAGCAAAAAG AAAAGATCAG CATGGGAAT GACAAAAAGT TTGTATGATG  
451 CGTGGTCAGG ATGGCTAGTA GTAACACTAA CAGGATTGGC ATCAGGGCA  
501 CTGGCCGGAT TAATAGACAT TGCTGCCGAT TGGATGACTG ACCTAAAGGA  
551 GGGCATTTGC CTTAGTGCCT GTGGTACAA CCACGAACAG TGCTGTTGG  
601 GATCTAATGA AACAAACATTG AAAGAGAGGG ATAAATGTCC ACAGTGGAA  
651 ACATGGGCAG AATTAATCAT AGGTCAAGCA GAGGGTCCTG GTTCTTATAT  
701 CATGAAC TAC ATAATGTACA TCTTCTGGC CTTGAGTTT GCCTTTCTTG  
751 CAGTTCCCT GGTAAAGGTA TTTGCTCCAT ATGCCTGTGG CTCTGGAATT  
801 CCAGAGATTA AAACATTAAAGTGGATTC ATCATCAGAG GTTACTTGGG  
851 AAAATGGACT TTAATGATTA AAACCATCAC ATTAGTCCTG GCTGTGGCAT  
901 CAGGTTGAG TTTAGGAAAAA GAAGGTCCCC TGGTACATGT TGCTGTTGC  
951 TGCGAAATA TCTTTTCTA CCTCTTCCA AAGTATAGCA CAAACGAAGC  
1001 TAAAAAAAGG GAGGTGCTAT CAGCTGCCTC AGCTGCAGGG GTTTCTGTAG  
1051 CTPTTGGTGC ACCAATTGGA GGAGTTCTT TTAGCCTGGA AGAGGTTAGC  
1101 TATTATTTCT CTCTCAAAAC TTTATGGAGA TCATTTTTG CTGCTTTAGT  
1151 GGCTGCATT TTTTGAGGT CCATCAATCC ATTTGGTAAC AGCCGCTG  
1201 TCCTTTTTA TGTGGAGTAT CATAACCAT GGTACCTTT TGAACTGTTT  
1251 CCTTTTATTC TTCTAGGGGT ATTGGAGGG CTTGGGGAG CTTTTTCAT  
1301 TAGGCAATAA ATGCCCTGGT GTCGTCGACG CAAGTCCACG AAATTGGA  
1351 AGTATCCCCT TCTGGAAGTC ATTATTGTT CAGCCATTAC TGCTGTGATA  
1401 GCCTTCCCTA ATCCATACAC TAGCTAAC ACCAGTGAAC TGATCAAAGA  
1451 GCTTTTACA GACTGTGGTC CCCTGGATC CTCTCTCTT TGTGACTACA  
1501 GAAATGACAT GAAATGCCAGT AAAATTGCG ATGACATTCC TGATCGTCCA  
1551 GCAGGCATTG GAGTATATTG AGCTATATGG CAGTTATGCC TGGCACTCAT  
1601 ATTTAAAATC ATAATGACAG TATTCACTT TGGCATCAAG GTTCCATCAG  
1651 GCTTGTTCAT CCCCAGCATG GCCATTGGAG CGATCGCAGG AAGGATTG  
1701 GGGATTGCGG TGGAGCAGCT TGCTACTAT CACCACGACT GTTTTATCTT  
1751 TAAGGAGTGG TGTGAGGTCG GGGCTGATTG CATTACACCT GGCCTTATG  
1801 CCATGGTGG TGCTGCTGCA TGCTTAGGTG GTGTGACAAG AATGACTGTC  
1851 TCCCTGGTGG TTATTGTTT TGAGCTTACT GGAGGCTTGG AATATATTGT  
1901 TCCCCTTATG GCTGCACTCA TGACCACTAA ATGGGTTGGA GATGCCTT  
1951 GCAGGAAAGG CATTATGAA GCACACATCC GATTAATGG ATACCCTT  
2001 TTGGATGCAA AAAAGAAATT CACTCATACC ACCCTGGCTG CTGACGTTAT  
2051 GAGACCTCGA AGGAATGATC CTCCCTTAGC TGTCTGACA CAGGACAATA  
2101 TGACAGTGG A TGATATAGAA AACATGATTA ATGAAACCG AGCTACATG  
2151 TTTCCTGTCA TAATGTCAAA AGAATCTAG AGATAGTGG GTTTGCCCT  
2201 CAGAAGAGAC CTGACAATTG CAATAGAAAG TGCCAGGAA AAACAAGAAG  
2251 GTATCGTTGG CAGTTCTCGG GTGTGTTTG CACAGCACAC CCCATCTCT  
2301 CCAGCAGAAA GTCCCTCGGG ATTGAAGCTT CGAACATTC TTGACATGAG  
2351 CCCTTTACA GTGACAGACCC ACACCCCAAT GGAGATTG TGGAATATT  
2401 TCCGAAAGCT GGGACTGAGG CAGTGCCTTG TAACTCACAA TGGGCGCCTC  
2451 CTTGGCATTAA TAACAAAAAA AGATATCCTC CGGCATATGG CCCAGACGGC  
2501 AAACCAAGAC CCCGCTCAA TAATGTCAA CTGAATCTCA CAGATGAGGA  
2551 GAGAGAAGAA ACGGAAAGAGG AAGTTTATTG GTTGAATAGC ACAACTCTT  
2601 AACCTGAGGG AGTCATCTAC TTTTTTTCTC TCCTTACAA AAAAGAAAG  
2651 GAAATATAAA AGCCGGGTTT TTGCAACATG GTTGCAAAT AATGCTGGTG  
2701 GAATGGAGGA GTTGGTTGGG GAGGGAAAGG AGAGAGAAGG AAAGGAGTGA  
2751 GGTATTCCC GTCTAACAGA AAGCAGCGTA TCAACTCTA TTGTTCTGCA  
2801 CTGGATGCAT TCAGCTGAGG ATGTGCCTGA TAGTGCAGGC TTGCGCCTCA  
2851 ACAGAGATGA CAGCAGAGTC CTCGAGCACC TGGCCTGTTG CTCCAACATT  
2901 GCAAAGACAC ATTATCAGTC CCTATTCTA GAGGGATTAC TTTGAATTGA  
2951 GCCATCTATA AAACTGCAAG GTCTGCCCT TTTTTTAAT CAAAACGT  
3001 CTGTTAATT CATGAATTGT ATAGTTAAC ATTACCTTTC TACATTCCAG  
3051 AAGAGCCTTT ATTCTCTCTCT CTCTCTCTCT CTCTCTACTG  
3101 AGCTGTAACA AAGCCTCTTT AAATCGGTGT ATCCTTTGA AGCAGTCCTT

3151 TCTCATATTG AGATGTACTG TGATTTACT GAGGTTCAT CACAAGAAGG  
3201 GAGTGTTCCT TGTGCCATTA ACCATGTAGT TTGTACCATC ACTAAATGCT  
3251 TGGAACAGTA CACATGCACC ACAACAAAGG CTCATCAAAC AGGTAAAGTC  
3301 TCGAAGGAAG CGAGAACGAA ATCTCTCATT GTGTGCCGTG TGGCTAAAAA  
3351 CCGAAAACAA TGAAGCTTGG TTTTAAAGGA TAAAGTTTC TTTTTTGT  
3401 TCCTCTCAGA CTTTATGGAT AATGTGACCG GGTCTTATGC AAATTTCTA  
3451 TTTCTAAAC TACTACTATG ATATACAAGT GCTGTTGAGC ATAATTAAAT  
3501 AAAATGCTGC TGCTTGACA GTAAAGAGAA AAAAAAAA AAAAAAAA  
3551 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA  
3601 AAAAAAAA AAAAAAAA AAAAAA (SEQ ID NO:1)

**FEATURES:**

5'UTR: 1-158  
Start Codon: 159  
Stop Codon: 2532  
3'UTR: 2535

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**HOMOLOGOUS PROTEINS:****Top BLAST Hits:**

		Score	E
CRA 18000005109762	/altid=gi 2599548 /def=gb AAB95161.1  (AF029...	1575	0.0
CRA 18000005109763	/altid=gi 2599550 /def=gb AAB95162.1  (AF029...	1573	0.0
CRA 18000005227216	/altid=gi 4762023 /def=gb AAD29440.1 AF14277...	1572	0.0
CRA 18000004989660	/altid=gi 4502869 /def=ref NP_001820.1  chlo...	1570	0.0
CRA 18000005231972	/altid=gi 8134363 /def=sp Q9R279 CLC3_CAVPO ...	1561	0.0
CRA 18000004989700	/altid=gi 6680948 /def=ref NP_031737.1  chlo...	1560	0.0
CRA 18000004978791	/altid=gi 1705905 /def=sp P51792 CLC3_RAT CH...	1560	0.0
CRA 1000685681515	/altid=gi 6634696 /def=emb CAA71072.2  (Y0994...	1559	0.0
CRA 18000004989661	/altid=gi 1705903 /def=sp P51790 CLC3_HUMAN ...	1558	0.0
CRA 18000005226296	/altid=gi 4753144 /def=gb AAB88634.2  (U8346...	1556	0.0

**EST:**

		Score	E
gi 10993825	/dataset=dbest /taxon=96...	1562	0.0
gi 10934924	/dataset=dbest /taxon=96...	1336	0.0
gi 10952244	/dataset=dbest /taxon=96...	1251	0.0
gi 12383593	/dataset=dbest /taxon=96...	1205	0.0
gi 6591096	/dataset=dbest /taxon=9606 ...	1170	0.0
gi 10251711	/dataset=dbest /taxon=96...	1104	0.0
gi 2321385	/dataset=dbest /taxon=9606 ...	1045	0.0
gi 5594360	/dataset=dbest /taxon=9606 ...	975	0.0
gi 5422132	/dataset=dbest /taxon=9606 ...	965	0.0
gi 10327969	/dataset=dbest /taxon=96...	963	0.0

**EXPRESSION INFORMATION FOR MODULATORY USE:****library source:**

gi|10993825 Neuronal precursor cells-teratocarcinoma  
 gi|10934924 Whole embryo-mainly head  
 gi|10952244 Neuronal precursor cells-teratocarcinoma  
 gi|12383593 Small intestine-duodenal adenocarcinoma  
 gi|6591096 Lung-small cell carcinoma  
 gi|10251711 Breast-normal  
 gi|2321385 Schwannoma tumor  
 gi|5594360 Brain-tumor  
 gi|5422132 Testis  
 gi|10327969 Lung-large cell carcinoma

1 MDASSDPYLP YDGGGGDNIPL RELHKRGTHY TMTNGGSINS STHLLDLLDE  
51 PIPGVGTYDD FHTIDWREK CKDRERHRRRI NSKKKESAWE MTKSLYDAWS  
101 GVLVVTLTGL ASGALAGLID IAADWMTDLK EGICL SALWY NHEQCCWGSN  
151 ETTFEERDKC PQWKTWAELI IGQAE GPGSY IMNYIMYIFW ALSFAFLAVS  
201 LVKVFAPYAC GSGIPEIKTI LSGFIIRGYL GKWTLMIKTI TLVLAVASGL  
251 SLGKEGPLVH VACCCGNIFS YLFPKYSTNE AKKREVL SAA SAAGVSVAFG  
301 APIGGVLFSL EEVSYYFPLK TLWRSFFAAL VAAFVLRSIN PFGNSRLVLF  
351 YVEYHTPWYL FELFPFILLG VFGGLWGAFF IRANIAWCRRKSTKFGKYP  
401 VLEVIIVAAI TAVIAFPNPY TRLNTSELIK ELFTDCGPLE SSSLCDYRND  
451 MNASKIVDDI PDRPAGIGVY SAIWQLCLAL IFKIIMTVFT FGKVP SGLF  
501 IPSMAIGAIA GRIVGIAVEQ LAYYHHDWFI FKEWCEVGAD CITPGLYAMV  
551 GAAACLGGVT RMTVSLVVIV FELTGGL EYI VPLMAAVMTS KWVGDAFGRE  
601 GIYEAHIRLN GYPFLDAKEE FTHTTLLAADV MRPRRNDPPL AVLQDNMTV  
651 DDIENMINET SYNGFPVIMS KESQRLVGFA LRRDLTIAIE SARKKQEGIV  
701 GSSRVCFQAQH TPSLPAESPR PLKLR SILD M SPFTVTDHTP MEIVVDIFRK  
751 LGLRQCLVTH NGRLLGIITK KDILRHMAQT ANQDPASIMF N (SEQ ID NO:2)

**FEATURES:**

**Functional domains and key regions:**

[1] PDOC00001 PS00001 ASN\_GLYCOSYLATION

N-glycosylation site

Number of matches: 5

1	90-93	NETT
2	364-367	NTSE
3	392-395	NASK
4	587-590	NMTV
5	598-601	NETS

[2] PDOC00004 PS00004 CAMP\_PHOSPHO\_SITE

cAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 3

1	24-27	KKES
2	330-333	RRKS
3	331-334	RKST

[3] PDOC00005 PS00005 PKC\_PHOSPHO\_SITE

Protein kinase C phosphorylation site

Number of matches: 8

1	22-24	SKK
2	333-335	STK
3	529-531	TSK
4	613-615	SQR
5	631-633	SAR
6	642-644	SSR
7	658-660	SPR
8	709-711	TKK

[4] PDOC00006 PS00006 CK2\_PHOSPHO\_SITE  
Casein kinase II phosphorylation site

Number of matches: 13

1	27-30	SAWE
2	34-37	SLYD
3	92-95	TTFE
4	93-96	TFEE
5	105-108	TWAE
6	217-220	STNE
7	249-252	SLEE
8	383-386	SLCD
9	589-592	TVDD
10	666-669	SILD
11	674-677	TVTD
12	679-682	TPME
13	709-712	TKKD

[5] PDOC00008 PS00008 MYRISTYL  
N-myristoylation site

Number of matches: 18

1	49-54	GLASGA
2	53-58	GALAGL
3	72-77	GICLSA
4	88-93	GSNETT
5	189-194	GLSLGK
6	206-211	GNIFSY
7	234-239	GVSVAF
8	240-245	GAPIGG
9	245-250	GVLFSL
10	310-315	GVFGGL
11	313-318	GGLWGA
12	314-319	GLWGAF
13	408-413	GVYSAI
14	447-452	GAIAGR
15	491-496	GAAACL
16	541-546	GIYEAH
17	638-643	GIVGSS
18	692-697	GLRQCL

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	99	119	1.810	Certain
2	182	202	2.131	Certain
3	233	253	1.398	Certain
4	256	276	1.019	Certain
5	290	310	1.770	Certain
6	321	341	0.797	Putative
7	361	381	2.093	Certain
8	400	420	1.539	Certain
9	473	493	1.739	Certain
10	496	516	1.218	Certain
11	540	560	1.568	Certain
12	570	590	0.975	Putative

**BLAST Alignment to Top Hit:**

>CRA|18000005109762 /altid=gi|2599548 /def=gb|AAB95161.1| (AF029346)  
chloride channel protein 3 [Homo sapiens] /org=Homo  
sapiens /taxon=9606 /dataset=nraa /length=818  
Length = 818

Score = 1572 bits (4026), Expect = 0.0  
Identities = 764/765 (99%), Positives = 764/765 (99%)

Query: 27 GTHYTMTNGGSINSSTHLLDEPIPGVGTYDDFHTIDWVREKCKDRERHRRINSKKKE 86  
GTHYTMTNGGSINSSTHLLDEPIPGVGTYDDFHTIDWVREKCKDRERHRRINSKKKE  
Sbjct: 54 GTHYTMTNGGSINSSTHLLDEPIPGVGTYDDFHTIDWVREKCKDRERHRRINSKKKE 113

Query: 87 SAWEMTKSLYDAWSGWLVVTLTGLASGALAGLIDIAADWMTDLKEGICL SALWYNHEQCC 146  
SAWEMTKSLYDAWSGWLVVTLTGLASGALAGLIDIAADWMTDLKEGICL SALWYNHEQCC  
Sbjct: 114 SAWEMTKSLYDAWSGWLVVTLTGLASGALAGLIDIAADWMTDLKEGICL SALWYNHEQCC 173

Query: 147 WGSNETTFEERDKCPQWKTWAELIIGQAEGPGSYIMNYIMYIFWALSFAFLAVSLVKVFA 206  
WGSNETTFEERDKCPQWKTWAELIIGQAEGPGSYIMNYIMYIFWALSFAFLAVSLVKVFA  
Sbjct: 174 WGSNETTFEERDKCPQWKTWAELIIGQAEGPGSYIMNYIMYIFWALSFAFLAVSLVKVFA 233

Query: 207 PYACGSGIPEIKTILSGFIIRGYLGKWTLMIKTTITLVLAVASGLSLGKEGPLVHVACCG 266  
PYACGSGIPEIKTILSGFIIRGYLGKWTLMIKTTITLVLAVASGLSLGKEGPLVHVACCG  
Sbjct: 234 PYACGSGIPEIKTILSGFIIRGYLGKWTLMIKTTITLVLAVASGLSLGKEGPLVHVACCG 293

Query: 267 NIFSYLFPKYSTNEAKKREVLSAASAAGVSVAFGAPIGGVLFSLEEVSYYFPLKTLWRSF 326  
NIFSYLFPKYSTNEAKKREVLSAASAAGVSVAFGAPIGGVLFSLEEVSYYFPLKTLWRSF  
Sbjct: 294 NIFSYLFPKYSTNEAKKREVLSAASAAGVSVAFGAPIGGVLFSLEEVSYYFPLKTLWRSF 353

Query: 327 FAALVAAFVLR SINPFGNSRLVLFYVEYHTPWYLFELFPFILLGVFGGLWGAFFIRANIA 386  
FAALVAAFVLR SINPFGNSRLVLFYVEYHTPWYLFELFPFILLGVFGGLWGAFFIRANIA  
Sbjct: 354 FAALVAAFVLR SINPFGNSRLVLFYVEYHTPWYLFELFPFILLGVFGGLWGAFFIRANIA 413

Query: 387 WCRRRKSTKFGKYPVLEVIIVAAITAVIAFPNPYTRLNTSELIKELFTDCGPLESSLCD 446  
WCRRRKSTKFGKYPVLEVIIVAAITAVIAFPNPYTRLNTSELIKELFTDCGPLESSLCD  
Sbjct: 414 WCRRRKSTKFGKYPVLEVIIVAAITAVIAFPNPYTRLNTSELIKELFTDCGPLESSLCD 473

Query: 447 YRNDMNASKIVDDIPDRPAGIGVYSAIWQLCLALIFKIIIMTVFTFGIKVPSGLFIPSMAI 506  
YRNDMNASKIVDDIPDRPAGIGVYSAIWQLCLALIFKIIIMTVFTFGIKVPSGLFIPSMAI  
Sbjct: 474 YRNDMNASKIVDDIPDRPAGIGVYSAIWQLCLALIFKIIIMTVFTFGIKVPSGLFIPSMAI 533

Query: 507 GAIAGRIVGIAVEQLAYYHHDWFIFKEWCEVGADCITPGLYAMVGAACLGGVTRMTVSL 566  
GAIAGRIVGIAVEQLAYYHHDWFIFKEWCEVGADCITPGLYAMVGAACLGGVTRMTVSL  
Sbjct: 534 GAIAGRIVGIAVEQLAYYHHDWFIFKEWCEVGADCITPGLYAMVGAACLGGVTRMTVSL 593

Query: 567 VVIVFELTGGLEYIVPLMAAVMTSKWVGDAFGREGIYEAHIRLNGYPFLDAKEEFTHTTL 626  
VVIVFELTGGLEYIVPLMAAVMTSKWVGDAFGREGIYEAHIRLNGYPFLDAKEEFTHTTL  
Sbjct: 594 VVIVFELTGGLEYIVPLMAAVMTSKWVGDAFGREGIYEAHIRLNGYPFLDAKEEFTHTTL 653

Query: 627 AADVMRPLRNDPPLAVLTQDNMTVDDIENMINETS YNGFPVIMS KESQRLVG FALRRDLT 686  
AADVMRP RNDPPLAVLTQDNMTVDDIENMINETS YNGFPVIMS KESQRLVG FALRRDLT  
Sbjct: 654 AADVMRPRRNDPPLAVLTQDNMTVDDIENMINETS YNGFPVIMS KESQRLVG FALRRDLT 713

Query: 687 IAIESARKKQEGIVGSSRVCFAQHTPSLPAESPRPLKLR SILDMS PFTVTDHTPMEIVVD 746  
IAIESARKKQEGIVGSSRVCFAQHTPSLPAESPRPLKLR SILDMS PFTVTDHTPMEIVVD  
Sbjct: 714 IAIESARKKQEGIVGSSRVCFAQHTPSLPAESPRPLKLR SILDMS PFTVTDHTPMEIVVD 773

Query: 747 IFRKLGLRQCLVTHNGRLLGIITKKDILRHMAQTANQDPASIMFN 791  
IFRKLGRLRQCLVTHNGRLLGIITKKDILRHMAQTANQDPASIMFN  
Sbjct: 774 IFRKLGLRQCLVTHNGRLLGIITKKDILRHMAQTANQDPASIMFN 818 (SEQ ID NO:4)

>CRA|18000004989660 /altid=gi|4502869 /def=ref|NP\_001820.1| chloride  
channel 3; CLC-3 [Homo sapiens] /org=Homo sapiens  
/taxon=9606 /dataset=nraa /length=820  
Length = 820

Score = 1567 bits (4013), Expect = 0.0  
Identities = 764/767 (99%), Positives = 764/767 (99%), Gaps = 2/767 (0%)

Query: 27 GTHYMTNGGSINSSTHLLDEPIPGVGTYDDFHTIDWVREKCKDRERHRRINSKKKE 86  
GTHYMTNGGSINSSTHLLDEPIPGVGTYDDFHTIDWVREKCKDRERHRRINSKKKE  
Sbjct: 54 GTHYMTNGGSINSSTHLLDEPIPGVGTYDDFHTIDWVREKCKDRERHRRINSKKKE 113

Query: 87 SAWEMTKSLYDASGWLVVTLTGLASGALAGLIDIAADWMTDLKEGICLSALWYNHEQCC 146  
SAWEMTKSLYDASGWLVVTLTGLASGALAGLIDIAADWMTDLKEGICLSALWYNHEQCC  
Sbjct: 114 SAWEMTKSLYDASGWLVVTLTGLASGALAGLIDIAADWMTDLKEGICLSALWYNHEQCC 173

Query: 147 WGSNETTFEERDKCPQWKTWAELIIGQAEGPGSYIMNYIMYIFWALSFAFLAVSLVKVFA 206  
WGSNETTFEERDKCPQWKTWAELIIGQAEGPGSYIMNYIMYIFWALSFAFLAVSLVKVFA  
Sbjct: 174 WGSNETTFEERDKCPQWKTWAELIIGQAEGPGSYIMNYIMYIFWALSFAFLAVSLVKVFA 233

Query: 207 PYACGSGIPEIKTILSGFIIRGYLGKWTLMIKTITLVLAVASGLSLGKEGPLVHVACCCG 266  
PYACGSGIPEIKTILSGFIIRGYLGKWTLMIKTITLVLAVASGLSLGKEGPLVHVACCCG  
Sbjct: 234 PYACGSGIPEIKTILSGFIIRGYLGKWTLMIKTITLVLAVASGLSLGKEGPLVHVACCCG 293

Query: 267 NIFSYLFPKYSTNEAKKREVLSAASAAGVSVAFGAPIGGVLFSLEEVSYYFPLKTLWRSF 326  
NIFSYLFPKYSTNEAKKREVLSAASAAGVSVAFGAPIGGVLFSLEEVSYYFPLKTLWRSF  
Sbjct: 294 NIFSYLFPKYSTNEAKKREVLSAASAAGVSVAFGAPIGGVLFSLEEVSYYFPLKTLWRSF 353

Query: 327 FAALVAAFVLRSPNPGNSRLVLFYVEYHTPWYLFELFPPILLGVFGGLWGAFFIRANIA 386  
FAALVAAFVLRSPNPGNSRLVLFYVEYHTPWYLFELFPPILLGVFGGLWGAFFIRANIA  
Sbjct: 354 FAALVAAFVLRSPNPGNSRLVLFYVEYHTPWYLFELFPPILLGVFGGLWGAFFIRANIA 413

Query: 387 WCRRRKSTKFGKYPVLEVIIVAAITAVIAFPNPYTRLNTSELIKELFTDCGPLESSLCD 446  
WCRRRKSTKFGKYPVLEVIIVAAITAVIAFPNPYTRLNTSELIKELFTDCGPLESSLCD  
Sbjct: 414 WCRRRKSTKFGKYPVLEVIIVAAITAVIAFPNPYTRLNTSELIKELFTDCGPLESSLCD 473

Query: 447 YRNDMNASKIVDDIPDRPAGIGVYSAIWQLCLALIFKIIIMTVFTFGIKVPSGLFIPSMAI 506  
YRNDMNASKIVDDIPDRPAGIGVYSAIWQLCLALIFKIIIMTVFTFGIKVPSGLFIPSMAI  
Sbjct: 474 YRNDMNASKIVDDIPDRPAGIGVYSAIWQLCLALIFKIIIMTVFTFGIKVPSGLFIPSMAI 533

Query: 507 GAIAGRIVGIAVEQLAYYHHDWFIFKEWCEVGADCITPGLYAMVGAACLGGVTRMTVSL 566  
GAIAGRIVGIAVEQLAYYHHDWFIFKEWCEVGADCITPGLYAMVGAACLGGVTRMTVSL  
Sbjct: 534 GAIAGRIVGIAVEQLAYYHHDWFIFKEWCEVGADCITPGLYAMVGAACLGGVTRMTVSL 593

Query: 567 VVIVFELTGGLEYIVPLMAAVMTSKWVGDAFGREGIYEAHIRLNGYPFLDAKE--EFTHT 624  
VVIVFELTGGLEYIVPLMAAVMTSKWVGDAFGREGIYEAHIRLNGYPFLDAKE EFTHT  
Sbjct: 594 VVIVFELTGGLEYIVPLMAAVMTSKWVGDAFGREGIYEAHIRLNGYPFLDAKEEFTHT 653

Query: 625 TLAADVMRPLRNDPPLAVLTQDNMTVDDIENMINETSNGFPVIMSKESQLVGFALRRD 684  
TLAADVMRP RNDPPLAVLTQDNMTVDDIENMINETSNGFPVIMSKESQLVGFALRRD  
Sbjct: 654 TLAADVMRPRNDPPLAVLTQDNMTVDDIENMINETSNGFPVIMSKESQLVGFALRRD 713

Query: 685 LTIAIESARKKQEGIVGSSRVCFAQHTPSLPAESPRPLKLRSLIDMSPFTVTDHTPMEIV 744  
LTIAIESARKKQEGIVGSSRVCFAQHTPSLPAESPRPLKLRSLIDMSPFTVTDHTPMEIV  
Sbjct: 714 LTIAIESARKKQEGIVGSSRVCFAQHTPSLPAESPRPLKLRSLIDMSPFTVTDHTPMEIV 773

Query: 745 VDIFRKLGRLQCLVTHNGLLGIITKKDILRHMAQTANQDPASIMFN 791  
VDIFRKLGRLQCLVTHNGLLGIITKKDILRHMAQTANQDPASIMFN  
Sbjct: 774 VDIFRKLGRLQCLVTHNGLLGIITKKDILRHMAQTANQDPASIMFN 820 (SEQ ID NO:5)

>CRA|1000685681515 /altid=gi|6634696 /def=emb|CAA71072.2| (Y09941)  
 putative chloride channel CLC-3 [Xenopus laevis]  
 /org=Xenopus laevis /taxon=8355 /dataset=nraa  
 /length=791  
 Length = 791

Score = 1559 bits (3993), Expect = 0.0  
 Identities = 745/791 (94%), Positives = 771/791 (97%)

Query: 1 MDASSDPYLPYDGGGDNIPLRELHKRGTHYTMTNGGSINSSTHLLDLLDEPIPGVGTYDD 60  
 MD SSDPYLPYDGGGDNIPLR+LHKRGTHYT+TNGG+INS+THLLDLLDEPIPGVGTYDD  
 Sbjct: 1 MDISSDPYLPYDGGGDNIPLRDLHKRGTHYTVTNGGAINSTTHLLDLLDEPIPGVGTYDD 60  
 (SEQ ID NO:6)

**Hmmer search results (Pfam):**

Model	Description	Score	E-value	N
CE00039	CE00039 chloride_channel	1671.9	0	1
CE00420	E00420 CLC	1288.1	0	2
PF00654	Voltage gated chloride channels	1172.4	0	1
PF00571	CBS domain	78.1	7e-20	2

**Parsed for domains:**

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00654	1/1	71	622 ..	1	621 []	1172.4	0
PF00571	1/2	645	690 ..	11	54 .]	31.4	5.8e-07
CE00420	1/2	32	697 ..	1	729 [.	1174.4	0
PF00571	2/2	726	778 ..	1	54 []	47.4	2.2e-11
CE00420	2/2	722	791 .]	867	942 ..	110.6	6.5e-32
CE00039	1/1	60	791 .]	1	804 []	1671.9	0

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51 TGTTTATCTT TAAAATAAT TCAAATATGG CTACAAAATC TTTACAATAT  
101 GAAGCATTGT CAGTATTTAT TTTACCGGGG GGATTCCCC CATCAGTGAG  
151 TGCTGACTGT CATTTCATT CTTTATGATC AAGTTGAGA TCAGGAAAAAA  
201 CAAGTTAAGA GAGTGCCTAC AAATACCGGG AAAACTTGTG GATAGATTT  
251 CATTTTTAT GTAAAGACAT ATAAGAACAT GAATGGTATA AAAACAAAAT  
301 CCTTTATAAA TGCCATACAA TTATATATT AGAAAATTA TATGGTGGTA  
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54751 TTTCAACGGT GGAGTGGAAAG TAGGCAGCAG GACAGAAGAA CTTGAAGCAG  
54801 AGCACACTGG AGAGGAGAAA TAAACAAAGC CTTTATGAAT AAAACAAACCC  
54851 CCCAATATCA GTCTGTGTGC ATTATGAGCA TAATGTACT TTCATCTCAT  
54901 CTGTAATGTT CATGACTTTT CTAGAAAATT ATACTTTAAC ATGAGAAAAG  
54951 AAAAGAACCC AGCTAATTCA TAGGGATGGA GGACACAGCA TAGTCAAAGC  
55001 AAGAATGAAA CTCTTTTAG TGCCACCTCC AGTGCAGAAT AAGTAACATT  
55051 CAGCAGAGGC AGTTTCATT TGATAATGGA TTCCATAAT AAACCTGCGT  
55101 CAGAATTGTG GCAGGTTTA AAATCCGTA TTCAAACCC ACTTCCTTAG  
55151 CCCCCAAGTT AGAAAACAGC TTCAGTAAAG AAAATTGTAC GATGATATAA  
55201 CTTTACAAA AAATAATTTC TTTCCATGAA GATGATATAT TATTGTTGAC  
55251 TTCTAATTCA ATCAAATATA ACAATTGCT AAATGGCTTT TCAGTTGACT  
55301 CCTTCTTGG TTAAGGAGAA GATAGGAAAA AATGAAGGGA TCAGAAGTCA  
55351 TAGGATACAT TAATTTTTT TATCTCTGAA TAAACAGGTT GCCTACTTAA  
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55751 AGTCAGCTCC CAGGTGGAA AGTCTGTCT ATGGTATAGT CACAAATATA  
55801 GGATCAGTCA ATCAAATTT ACATTTACTA AGGAATAAGA AAGATGTCA  
55851 CTGCTGCTC TTGCCAAAC AGTGCACATT GTAAAATAA CCTCAAAGTT  
55901 GGAAAAGAGG TGCTGAAAGA TCTCCAGCAT GAAAGCATGT TGAGCTTACA  
55951 GTGCTTCTTT TCCTAGGGAA GAGTGGACCT AACCTGCATG GAGCACTGCA  
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56051 AGTACAATAA TAAGTTCTA GATATTTGC TATTTACTCT TTCAGCCAAT  
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56201 ACCTTCTCT ATACAAAT CTTTTATATT TATATAACTG CTAAGGACAA  
56251 ATAAATACTC ATGTATTTAA AATGTATACA TTGATAATT TTTTTCCAC  
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56351 GAAACAGATG TCACGGGGGT TGTGGAGACC TTAATGCACA GAATTGATT  
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56451 CTGTTCTCC ACACCTCTT CTTTAGGACC CTTCATTTCC ACTATATATT  
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60151 CTGTTTCAGG ATTGTCCTGG GGATCATCAC AAAGAAGAAC ATATTAGAGC  
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60301 CTGTTGAGTT CTGTCCTTCC CAGATATCTG CTGAACAAAA ATATCCTACT  
60351 ATGCTGCCA TTACATTGT ATCTGATAAA ATGTCGCTGT AAGATAAATT  
60401 TAGATATGTG TAAAATCCA TTTATAGAAA GTAAGCAAAA GTTAACATCT  
60451 CTCATCAAAT CATTCAATTAC AATTTCAGAA CTGTAACAG TTTGGTAGTG  
60501 GAATAAGTGA ATATTATTGG ACATTCTAA AGTGAATATG GCAAATCTGT  
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60601 GTCTGACCCA TCCCCGCAAG CCCTTTTTT TTTTTTAAA TGTTTCCCGA  
60651 TCTTGTGGTA GTCTTATGGT AAATCTAACG TCCTAAAGGA TTTAAAGGA  
60701 GCTTAGCAAT TAGAACTGCT TACAGTTAA TGGATTTTT AATGGGCACA  
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61001 GCATAACATA AAAAATGTCT GGCTTAGCA ATTAATGCC GAAATTATT  
61051 TGCCCTGCAA TTGTCATACC TGTATGAAAC CTGTCGGAGT TTGCTTAAGT  
61101 GCACAACGTG TTATGTATTCTGTTGTTGAT TCAAATATT CACAAGTGT  
61151 TCATGCATCC TTTTTAAAAA AACTACTAAC CAGAATATTA TCGTAGCTAC  
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61951 TCCCTAGTCA TACATCCATC CAGTTTTGT TACTTTTTG TTGGCATAACA  
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62201 ATTTAGCTAT AGATTTAGCT TCTCCCTTTA TTTTCCCTTT TATTTCATAG  
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63251 TAATGTGACC GGGCTTATG CAAATTTCT ATTTCTAAA CTACTACTAT  
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64201 TGCAAACAGA CATTTCCTT TTTTTGGCT GGAGTGCAGT GGGGCATGGT  
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64301 CAGCCACCCA AGTAGCTGGC ACTACGGGCA CACCCACCA TGCCCAGCTA  
64351 ATTTTTGTG ATTTTAGTA GAGATGGGT TTTGCCATGC TGCCCAGGCT  
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65251 GAAATTGTTG TGCCTGGCTA ATTGGCAAT TAATTACCA ATATAATAAG  
65301 TGTAGCGCCT TTTTGAATA CCCTTTGTA GAAGGTATGA TGAGAATGGG  
65351 CAAGGGTGT (SEQ ID NO:3)

**FEATURES:**

Start: 2159  
Exon: 2159-2237  
Intron: 2238-22041  
Exon: 22042-22199  
Intron: 22200-30359  
Exon: 30360-30459  
Intron: 30460-31475  
Exon: 31476-31663  
Intron: 31664-32964  
Exon: 32965-33087  
Intron: 33088-34548  
Exon: 34549-34755

Intron: 34756-37975  
 Exon: 37976-38056  
 Intron: 38057-39552  
 Exon: 39553-40098  
 Intron: 40099-46366  
 Exon: 46367-46553  
 Intron: 46554-49237  
 Exon: 49238-49636  
 Intron: 49637-55445  
 Exon: 55446-55662  
 Intron: 55663-62274  
 Exon: 62275-62362  
 Stop: 62363

**CHROMOSOME MAP POSITION:**

Chromosome 4

**ALLELIC VARIANTS (SNPs):**

DNA

Position	Major	Minor	Domain
1275	T	C	Beyond ORF(5')
1456	T	C	Beyond ORF(5')
5893	G	A	Intron
6226	A	G	Intron
8866	T	G	Intron
10397	C	T	Intron
10621	T	-	Intron
19651	A	G T	Intron
19891	T	-	Intron
20272	C	A	Intron
20412	T	A	Intron
23340	A	G	Intron
29948	T	A	Intron
33579	A	C	Intron
40762	G	A	Intron
40936	T	C	Intron
45998	A	G	Intron
47771	T	C	Intron
48117	C	T	Intron
54563	T	G	Intron
58735	C	T	Intron
59643	C	A	Intron
61638	G	T	Intron
63291	G	C	Beyond ORF(3')
63463	A	G	Beyond ORF(3')
63636	G	A	Beyond ORF(3')
63998	T	C	Beyond ORF(3')

Context:

DNA

Position  
1275

GCATTTCAGGAGGAGAATCTCCAGTCTAGAGGAATCCTCTCAGAGGTAGCTATAAAATA  
 TTGAACCTGATCTTCATAAGCATTGTGCGGTTTTGTTTTGTTTAATGACAGTTT  
 TAAACAAGAAAGTTGCTTATTCTGAACCTCATAAAATTCTATTAAAGAGACAATT  
 CTGAATTCTATAACAATTCTAGAACAGTTGAGTACCTCACTTGAGACACATTGCT  
 AAAAGTTAAAAACACAAAACCCTATGAGATAAAATAGGAAGCTAGTAGAGATAGGAAAG  
 [T, C]  
 CCTCTGCTTAGTAAACCTTTTGTGCTAGTTAGACACATACAATAGTAAAGTTACTT  
 AGTACGTTGATAGTTCTTCTCTCAAAAGCTACAATGTCTACTAGCTAGTTCCCTC  
 AAGAAAGGAAACAAGAAGCCGCTGGAGGAGATTGGTAGTGGGATAAAACACTATTCAAC

	TCTTCAGTTATCGGTTTAAATCCTCAATGAAAGGCTGCTGTATTATAGAGTATTTT TTTTATTTAATAGACTAGAACCAAGTTCTGAGAAACCTTGGCATATTGTAGTT
1456	TGAATTTATAACAATTCAGAACAGTTGAGTACCTCACTTGAGACACATTTTGCTA AAAGTTAAAACACAAAACCCCTATGAGATAAAATAGGAAGCTAGTAGAGATAGGAAAGT CCTCTGCTTAGTAAACCTCTTTTGCCTAGTTAGACACATACAATAGTAAAGTTACTT AGTACGTTGATAGTTCTCTCCTCAAAAGCTACAATGCTTACTAGCTAGTTCCCTC AAGAAGGAAACAAGAACGCCCTGGAGGAGATTGGTAGTGGGATAAAACACTATTCAAC [T, C] CTTCAGTTATCGGTTTAAATCCTCAATGAAAGGCTGCTGTATTATAGAGTATTTT TTTTATTTAATAGACTAGAACCAAGTTCTGAGAAACCTTGGCATATTGTAGTT TTTTATGGCTATGACTCACATGACATTACTGTATAAAACTAGTACATTCTCTCGTAAAC CACACAAACTACTAGAGTGCTGCTCTACATTAGAAATGAAAAGGGCATT GTCTGCATTCAAATTCCTTTTACATCTCTGTATTACTTTCCCCTTATTTATC
5893	TCTAGTTGACAAGACTGAGGTAAGGAATTGTTAAGGAAAAGTCAGAATCCATCCAGATA TTGGCTCATACTTTAATCATGAGGCTAAACTGCTTCTCTCACACGTATCTCATAGTA ACTTGTGTTTAAGTCTGGTAGAACGATAAGAAGTTAAACACAGACAGAATCTGTGGA AGTTAGTAAATTCTAGTGAACGATAGAAATGATAGAAATCTCTCTCCCAAGTCC CAAGAACAGATTAGTCTGCTTTGACAAGTGTATCAAAGTAGACTGTTCTCACATACAC [G, A] GGGGACTCAATAGGCATTCTGGATATAAATAAAATGAGTAAATGCGATAACAGGAG GAAATGCCTAGTGTGTTGCTCTGGATTAGTTGATACAACAAAGGCAGCTTGTG AGTCAGTAGAGGGTAGTGTAGAAAGGTGAAGTGGAGTGGCAGATCCTAGAGGA CTAATGATGGCTTAAACCACAAAAGTGTGCGCTTGCATTGAA
6226	ATAAAATGACTAAATGCCATAACAGGAGGAAATGCCAGTGTGTTGCTCTGGATTAGTT TTGATACAACAAAGGCAGCTTGTGAGTCAGTAGAGAGGGTAGTGTAGAAAGTCGA AGTTGGAAGAGTGGCAGATCCTAGAGGACTAATGATGGCTAAACCACAAAAGTTCG CTTGCCATGAAATAAAAGTTGGGTCTTATTTTCAATTCTCCCTGAAATTATT TCTTGACATTCATTAGCTCAGCAGTGTATCTAAATAAGCTTTTGGTTCTATTATA [A, G] TAGAGGTTGTTCCCTTTCTCCCTTGAAAGTATCATTTTGACATTATTGAAA ATCCAGGTGTTATATGATATTCTATTGCCAGAGGGACATTCTGCAGGCTTTGTAAAA TGATTTTAGGATTAGCAGATACCTATTATATTATTGGCCCTAATATTATCCAACAG AAAATTAAACCTCTTCTAAAATTAACTCAAGTGTCTGTAATTAAAGGAACAC TAAAGATTCTTATTGGTGTAGAAACACTCCTGTTCTACACAGTAGTATAAAACAAA
8866	ACATGTAACCAACAATGAAATTATTTAGTGAATTGAGAATCAAAGTGTAGAGTTGA ATCCCTGTTCTACTACTTGCTAGCGGTGTGACCTTGGCCTGTTAACTCTGACACCTT GTTTCCAAATTATAAAGTGGAGATAATAATATCTGTCACATTGTGTTGTTGAGGAT TATATGAACTAATATATGTAATGCTCTGAGAACATGCTGTTACACATTAAGTTAATTA AAATTAGCTGTTCTACTGTTATTAGACATGAGCTAGATAACAGTGGCTCTACATG [T, G] GAAAGATTATTTAATTCTGATGTAGTCAGTTATCTATTGTTATTTGTCCCTT TTGCATTGATGTCATATCTAAAAACCTGCTAACTCAGGATCACAAAATTTACTCCTG TATTTATAATTAGCTCTTAGATCTAGGATCCATTAGCTAATTGTTATATGTTG TGTGAGGTAGGGTACGGTTCTTGTCACTTGACGTGAATGCCAGTTGTCAGCATCA TTTATTCAAAGACTATTCTTCTCACTAGAAAAAATTCTTTAAAGAATAATGAAT
10397	CCAGGCTCCCTGAACCTGGCTCAGATGATAGCCTCTGCCACAGCGTCCTGATT AGCTGGACTACAGGTGTGCAACACTACACGGCTTCTGATGAAATTAAATACCC AAATATTGAGCAGAAATAATAGCTGTTATTGTTTCTACTATCTGTCAGTATA GTATTAAATGTTACATAATTGCTCCAGTCCACATACAATACTCTAGTAGAAGTGG TAACAAACCAAGGTACTCAAAGAGGTTAATAAGTAACCTGCGCTGGATCACAGAACTAA [C, T] GGGAGGCAGGGCTGGAAATTGACTCTAGGTCTTCTGACCTCAAAGTGCAGTAAAGTCAT GGAATTCTCTACTAGGCCACCTGAGAAAAGTGTATCTTTCCAGTCTTTGTTA CTGTTTCTAGCCAGGAGATAGTAGAGTTAGGTAGTAGAATAGTAGTCAGTGGCATTGG TAGTCAGCCCTCCTTAAAGTTGATTGTTTTTTGTCTAAACTTGAAG CTACTAACCTTCAGGTCAACTTCTTATCATCCAAGAGCTGGATATTAGGTAGCAGAA
10621	CTCTAGTAGAAGTGGGTAACAAACCAAGGTACTCAAAGAGGTTAATAAGTAACCTGCGC

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 [T, -]  
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 TTGGCTAACCTGGATCTATGTGTTCTTAGCTGGGAGGAGAAGGTATCTGATTGA  
 TACCTCACCAAGGACTGCAGTGAGGGACAGAAGTTCTAAAATAATTGGTCT  
  
 19651      TTTATTTCTGCTACTATGGCAGAATTGAGTTGCAACTGTGTGGCATCCAAAGCCTA  
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 [A, G, T]  
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 CTTGAGCTATCTTTAATGT  
  
 19891      TTTATGCAAGTGTAGCTGCAAGAAAAAAACCTAGAAGTGAATTGCTAGGTTGAAGAGCA  
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 [T, -]  
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 AATTCAATTGCAATTACAGATAAAATTACTATTCAATTATCTTTACAAATCAT  
  
 20272      CAAAGATTATTTGACTCTAAAGGGAAACCCGCTGATGACAAGGCTGATTGAGAAGAG  
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 [C, A]  
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 20412      TTATTGTTCTACTGGACAGAATTCAATTGCAATTACCAATAAAATTACTATTCTA  
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 [T, A]  
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 23340      TTTTTTTTGGAGGTGGGGGACTGTCGCCATTCTGTTGCCAACTGGAGTGCAGTG  
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 AGTAGAGATGAAGTTGCCATGTTGGCGAGGCTAGTCTCAGACTCCTGGCCTCAAGTGA

	TTGGCTGACCTCAGCCTCCAAAGTAGAAAATCTTCTTGAAAAATAAAATTCAAATCTC [A, G] AAAGGCCCTATATAATTTGGTGGAAATTACTTGTCAATGAAAATGACTAATTACA CAAATTATAAGCTTCCATATTAATATATGTGTGAACCTGAAATTCAAATTTTATTA TATTGTATGAAAGGTACAGCCTGTGAGATTCACTAGATGGTATTACCTTAGGGCAT ATCTAAAATAAAACAGTACATGAAATCCAGTGCTTAATCCAGTGATTCTAAACTT TTGCTCTCAGATCCCCTTAAACTCTTAAAGATATTGAAGAGCTCCAAGGAGGTTG
29948	GACTCTACCAATGGGATCGGAGCTCCTCCAAACCTGCATATTAAAAGGCCTATAAGTTTG GGGGGTCCCTTGTCCACATGATTATTCTGTAATACATTGTATTGACATGGTATTA TTATACACAGATCCTGCTTTAAAGAACATTATAATCCACTTAACGTCTAGGACCAGAG AATGACCGATAATTCAAACCATATTGTCTTACAGAACATATATAAAAGATGGTTATGT GTACCAATTGAGGTTCAAATTGATTCAATTAAAACAATCTAGGCCAGATTATATAG [T, A] TTGTGGACCTTGCACCTCAAACTCAAGGTTCTTATTAAAATGCAGATCTGGCTGGC ACGGTGGCTCACACCTGTAATCCCAGCAGTTGGGAGGCCAAGGCAGGTAGATCATTGA GCTCAGAAGTTCAAGACCAGTCTGGCAACATAGCAGGCCAGTCTCATTGAAAGAAAA AAAATTTTTAATAAAAAAAGAACATCTGGGTAAGAACATGTAGTCTGGTTACA GGTATTAAACAACGTCTGTAATGTAGTATTGCTCCAGACTTACCTTCCATTATTT
33579	TTACTGTGAAGGCTGATTTTTTCTCACCACAAATTAAACACATGACTAGGC TTTCAGACTATTTAGTAAACATCAAGAGCCTGGAAGAAGTATCTGTGACCTAATGTT CTTGACGGTTAGTTGTTACTTGTCTTATGACCTGAAATTTTTTGAGACTG AGTCTTGTGCTGTCGCCAGACTGGAGTGCAGTGGCGAACATCAGCTCACTGCAACCTC TGCCTCCAGGCTCAAGCAATTCTGTCTCAGCCTCTGAGGAGTGCAGGC [A, C] CCTGTCACCATGCCCTGCTAATTGGCATTTTTGTTGTTGTTTTTTAGTAGAG ATGGGGTTTCAACCATGTTGCCAGGCTGGCTCAAACCTCAAACGATGATCACCG CCTCAGCCTCCAAAGTGTGGGATACAGGTGTGAGCCACACAGTGGCTATGACCT GATTTGATTCATTCACTTTATAATTACCTTTGATTAGATAAGTTAATTCTGTA ATTGGCCATTATGCTTGAGAAAGTAGTTAATCACAGTGGTCAACAGTACAAACTT
40762	ATCCATCACCTCAAGCATTATCCCTGTGTTACAAACAATTACAACACTCTTAATTA TTTTAAGGTACAATTAAATTATGAAATATAGTCAAAGACTTCTTCATTGACTAG CACCTAGGCTAAAAAAATTCAAGACACCTGGGCTCCTGGGATCAATCACGCATACTGTGTC TCTTGTGCTCACTCCC [G, A] CTGTCTCTCTCTTCTCGCTTCTCTCTCTCTCTCTGTGGTTCTAGGGTGG TGGCCTCAGGGATTGGATTCTTATATTAGCTCAGGATCCCAAGAGGGCTGTTTT AATGTAGCCAAAGAAGTCTGAGCGTGACTTGTGTTATTCTATTGAGGTAGTCAC AGAGGCCGACACAT
40936	TACAATTAAATTATTGAATATAGTCAAAGACTTCTCATTGACTAGCACCTAGGCT AAAAAAATTCAAGACACCTGGCTCCTGGGATCAATCACGCATACTGTGCTCTGTGCTC ACTCCCGTGTCTCTCTCTCTCTCGCTCCTTTCTCTCTGTGGTTCT AGGGTGGTGGCTCAGGGATTGGATTCTTATATTAGCTCAGGATCCCAAGAGGGC TGTGTTTAATGTAGCCAAAGAAGTCTGAGCGTGACTTGTGTTATTCTATTGAGG [T, C] AGTCACAGAGGCCGACCCACATTCAAGAGGGACATACACTGCTGGACAAGTGTAG AGAATTCACTGATCATGTTAAAACCACTTTATTAGTTCTATTGCTGCTGTAATAAA TTACCCACACTTAATGGCTAAAAGCCACACAAATTAAATCTTACAGTCTGCAACATC AAAAGTCTGAAACGGACTCACTGTGCTAAAATTAGGTGTTGAGGGCATTCTGGAGG CTGTTAGGAGAGAGTCTGTTTGTGCTTCTGGCTATTAAAAGCTGCCAGCATTCTT
45998	TGTATATCAGTCAAAATATTGGCAACTCTGATAAGTTGTCACCTAACATTGTACCCAC TTAAGATGAATAGCATCTACCAATTCCGTCAATTGTAATATAGGAGGACATAATCAC ATAATCTTGAAGTAAAAGACAGTGTCTAAAAGCTGAATCAGTTAAGTTTATGAAAATAC TTCATATTGTACTTTAAATTATATTGTTAATTCAATAGCTTGTGGTTACAAGT GGTTTGTTACGTGGATGAATTCTATAATGGTGAAGTCTAAGATTACTGCAACTGTC [A, G] CCCAAGTAGTATATTGTATCCAGCATATTGCTTTTTCTTTTTCTGGCTTCA TTTCACCATGGACTAATGAAAATTGTTAGGGACTGACATTAGGGCACCCCTGAGCTAC CTTGAGCTAAAGGAAATAACCCTTGAATTCTGTTGGCCTAGAGAATGTGGTTG

	TTTTGTAACTGAATTCATGGGATTGTTAAGGTACAAGATTGCTTTAGTTTATTGTA CTAGGATTTGCTATATTAAACATGTGAAAAGAATCAAAGTGTAGAAATAATGCA
47771	GAAGAGTAGAACATGAGGCTTATTAAAAGATTAGCAGAATTAAAGGAAAAGGTGACTT TGTTGAAGATTATAATGTGAAGACAAAGGAACGAGGATGGGAATAATTGTATTGATG AGGTTGAGAAAATTGACTCTAGAGAGTATTTGGCTACTTTGGAAATGAAGTTG GATTAGTGAGAAGGAACAGATTATGAAAAGACAAGAACCTGATTAATGTCAGGATGATT TTATATTGAG [T, C] TGGTCAGATTATGGCAGTCCTGGCTTGCCATTAGTTGATGACTTGAGAAAGTT CCTTCTTGAAGTTAATTTCTGTATATAAAAGTAATAACACCTGGTATCTGCTAGG TTGTTTGAGGATTATATGAGATAAAATGCATGCAAAACTGTTATAATAGTGCCTGGTA AAATAAGTGCCTAGTTTAAAAACAAGTCTTGAAACTGCTTAGGACATGCCTGGTATA GGTAGGTATGT
48117	GACTTTGAGAAAGTCCTCTTGAAGTTTAATTTCTGTATATAAAAGTAATAACACC TGGTGATCTGCTAGGTTGTTGAGGATTATGAGATAAAATGCATGCAAAACTGTTA TAATAGTGCCTGGTAAATAAGTGCCTAGTTAAAACAAGTCTTGAAACTGCTAG GACATGCCTGGTATAGGGTAGGTATGTAATACATAGTAGGTAGGATCTGTCCTTGCTA TTTTAGTAAAAAAACAAAAGGAAGAGCTTCAGCTTAATACAGTATGACTGACGAGCC [C, T] TGGTAGGTTTGAGCAAAAGAGCAACACAGTAAAAGTAGTACTTAGGAAAGATTAACAA GGGAACATGGCTTATACAGTGCATGGGGCTGGAGTCAGGAGGTAAGATAAAATGGT ATTATAATTAAGGAATAGCCAGGCACGATGGCACATGCATGTAATGCCAGCTACTGGAGA GGCTGAGGTGGGAGGATCATGGAGTCCAGGAGTTGAGGACAGCAGCTGGCAACTGAGTG AGACCCCAAATCTAAAAAATACAAGTAAAAAAGGAATAAAGTCAATGAGGGCTTGGACT
54563	GCTTTGTCACCCAGGCTGGAGTGTGGTATGATCATGGCTGACTGCAGCCCTGACCTT CCGGGCTCAAGTGATCTTCCACCTCAGCCTCCAAATTACTGGGACCACCAGCATGCTT GGCGATTTTTTTTTTTTTTGTAGAAGCAAGGTTCCCTATGTCAGGAA TGGTCTTGAACTTCTAGGCTCATGTGATACTCCTGCCTGGGCTCCAAAGTGTAGGAT TACAAGCCTGAGCCACCATGGCGGCCAAATATTTCACTATAACAAATATCATATCTG [T, G] ATATACTCAGTTAATACTAACTCAAAGTAGAAACATAAGCTGAATGACTATTATTATT TTCAGATTCTCCATTGAGTTCTCGTCTGTGATCTCTGAACCTTCTCCA TCTTGCCACTTCTGTCTAGCATTTTTTATCAGCAGTTCTTCACTAGATT TTAGTTCTTCAACGGTGGAGTGGAGTAGGCAGCAGGACAGAAGAACTGAAAGCAGAGC ACACTGGAGAGGAGAAATTAAACAAAGCCTTATGAATAAAACAACCCCCAATATCAGTC
58735	TGGGTTATGCCCTGTTAACTCTTACATCATTAGTTTAGGCCAAAAGGAAACAGCAAAT AATGTTTATATGAGCCACATTGCGTTGATTTCTTCCACTCTGTAAAATTACTAAA GCAGCACTGACTTTATTATGCTCAAATCGCTTCTCCATTATGTGTTCTCCAT CTTTAGGGTTTACTTATAAATACAGAGATTACTGTGAAATTCTAAATTGCCAC TGGGTCGTTATACATTGTAACCTCCTCACAGTATATTGTGATTTGGCAGAGTTAC [C, T] AATATAGATGATACTAACTGAAATTATCATTCTGTATAATTGGATAGAAAAGCATGAGT AAGAATTCAATTGGTATTATTTAATTGCAAGATTTCACATTCTGACTACA ACAATAAAATCAAATGAATTGATGGCTAAAAAGAAATCTCAAATGTTAGTCATG AAGAACATCTATTGAATGAGTGAATGTTCTTATATACTGCAATTGAGCTTTTT GGAGGGGGAGTTGCTCCATGCTGAGAACCTTAAAGGATGCAACATTATTTAAC
59643	GTTTATATTGCCACATTAATTCTTAAATAAAACAGTAACCATAGTTGTTTAATTA GCAATCTAATTATTTCTGTATCCTCATTATGAGAATTATGTCCATCACTTGCTTGA TGTGATAACAGTGACATGCTAAATGAGAAACAATTGTTATTAGAAAAAAATGCACAAAG TGAAAGTCCTTTAAATCCCTAAATCAAATACATTATTATAGCTTACTTTAAGAAGTGGC AGTCACAGCTCTGAACATTAGGGAGTGTCTTGGTCAGCATTATTATTTAGTGCA [C, A] ATTGCCTTAAATTGAAATTATAGTAAAATCCACGGGAGTTTTAAGTCTCCTC ACAGCCTTTGCTACCTTCAACAGGTAGATCCAGATGATAACTGCTGTGTTGACA TCATAGAAAATTAGAAAAATATTCTCTGAGGAAAGAACATTGAAATGAAACTCTACA TATCAGAGGTCTAGCTATGTTCAATTAAAGTTCTTTGACTTTGCTTGTAGTC ATCTTCATTCCAAACTTCTATAATTATTATTAAAGTTAAAGAAAAATAACCCACCA

61638	<p>AAAAAAAGAAAAACATTGATAAGTGCCTAGAAACTGGATTCTTTATAGATTGTTCT      TGGGGCTCTGATGTTGGATTGACGTTCTGTGCTGACCATTATGCATTTATCTT      AATAGTATGTGTTCATGAAGATTCTGATACAAGTGGCACTCTTAAATTATCTTGA      AAAATTGGTTAATTTGGTTAAAAAAGGAAAGTGGCTGGGTGCAGTGGCTACGCCTGT      AATCCCAGCACTTGGGAGGCCGGACGGGTGGATCACAAGGTCAAGGAGTTGAAGCCA      [G, T]      TCTGGCCAACATGGTAAACCCCTGTCCTACTGAAAATAATTGGGCATGGCACATG      CCTGTAATCCCAGCTACTTGGGAAGCTGAGGCAGGAGAATTGCTTGAACCGGGGACCCAG      GAGGCGGAGGGTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGCTACAGAGC      GAGACTCTGTCCTAAGAAATAAAATAAAATGAAAAGAGAAAATTGAGAGGA      TTGGTCATCTTACTGCTCTTCATGTGATGGAAATCAATTTCCTCTCAAATGG</p>
63291	<p>GAGATGTAAGTGTGATTTACTGAGGTTCATCACAGAAGGGAGTGTGATTTCTGTGCCATT      AACCAGTAGTTGTACCATCACTAAATGCTTGAACAGTACACATGCACCACAACAAAG      GCTCATCAAACAGGTAAGTCTCGAAGGAAGCGAGAACGAAATCTCTCATGTGTCGCGT      GTGGCTCAAACCGAAAACAATGAAGCTTGGTTAAAGGATAAAAGTTCTTTGTT      TTCCTCTAGACTTATGGATAATGTGACCGGGCTTATGCAAATTTCATTTCTAAA      [G, C]      TACTACTATGATATACAAGTGTGAGCATAATTAAATAAAATGCTGCTGTTGACA      GTAAAGAGAAGGAAGTATTCTGATTAGCTGTATCTGGTATTAAATTGCATGTTAAACACT      GGAATTTTAAAATTGAAATTAGATCAGTCATTCTTCTCAAGATATCTCATGG      CTGACACTGAAGAAGAAATGAAATTCTACACTTGCACTAAATGATATTTTCTCAA      AAATTTACCATCTTATTTATTTATGGATAAAATTATAAAACAGATCAGTTA</p>
63463	<p>TGTGCCGTGGCTCAAACCGAAAACAATGAAGCTTGGTTAAAGGATAAAAGTTCT      TTTTGTTTCTCTCAGACTTATGGATAATGTGACCGGGCTTATGCAAATTTCAT      TTCTAAAACTACTATGATATACAAGTGTGAGCATAATTAAATAAAATGCTGCT      GCTTGACAGTAAAGAGAAGGAAGTATTCTGATTAGCTGTATCTGGTATTAAATTGCATGT      TAAAACACTGGAATTAAAATTGAAATTAGATCAGTCATTCTTCTTCTCAAGAT      [A, G]      TCTCATGGCTGACACTGAAGAAGAAATGAAATTCTACACTTGCACTAAATGATATT      TTTCTAAAATTACCATCTTATTTATTTATGGATAAAATTATAAAACAG      ATCAGTTAATATTGCACTTAAGTAATTTCACCTTTAATGTGATTTTATAGAATAATT      CAGACTTACAAATACAGAGATATGAACAAAGTTACAGTGGGAAACAAAGGTTAAAAAA      GTTGTGGTCTCTCTGTGATCCAGTGTGACACATAACCTTCTGTATCTTCACTG</p>
63636	<p>TGCTGCTGCTTGTACAGTAAAGAGAAGGAAGTATTCTGATTAGCTGTATCTGGTATTAAT      TGCATGTTAAAACACTGGAATTTTAAAATTGAAATTAGATCAGTCATTCTTCTTCT      TCAAGATATCTCATGGCTGACACTGAAGAAGAAATGAAATTCTACACTTGCACTAAATG      ATATTTTTCTTAAACATTACCATCTTATTTATTTATGGATAAAATTATA      AAATACAGATCAGTTAATATTGCACTTAAGTAATTTCACCTTTAATGTGATTTTATA      [G, A]      AATAATTGAGACTTACAAATACAGAGATATGAACAAAGTTACAGTGGGAAACAAAGGTT      AAAAAGGTTGTGGTCTCTCTGTGATCCAGTGTGACATAACCTTCTGTATCT      TTCACTGCCATCCTCTGGATTATGTCTCTGACCTGTCCATTGACCCATTAACTGGAA      AGTTGAAAAACTACATTAACTGGAAGTTGAAAAACTACATTACTTGAGAATAAAACC      GAAAGTCGTGATACCTTCTTAAACCAAAATGAAACAAATAGAA</p>
63998	<p>AAAAAAAGGTTGTGGTCTCTCTGTGATCCAGTGTGACACATAACCTTCTGTATCT      TCACTGCCATCCTCTGGATTATGTCTCTGACCTGTCCATTGACCCATTAACTGAAA      GTTGAAGAAACTACATTAACTGGAAGTTGAAAAACTACATTACTTGAGAATAAAACCG      AAAGTCGTGATACCTTCTTAAACCAAAATGAAACAAATAGAA      TGCAAAGATAGCAGTTAAATTCTGAAAATACCTTGAATCTCGGGCTAGGTTA      [T, C]      GTCCATATTGAAAGTGGTCAGTGTGATGGTTGAACATTGGTGCAGGATGAGTTAAAGC      ACTGGATTATATTGGATTGGTTGGATTGTCTGTTTAATCACAGCCTTAATT      CACAATTGGCAAAGGCAGTTACTCAAAGGACTGGCTAAATATTCTGTAATTATGCATT      TTTGATAGGAAATGAAATTGGTCAAACAGACATTCTTGGCTGGAGTGCA      GTGGGGCATGGCTTGGCTCACTGCAGCGTTGACCACCTGGCTCAAGTGATACTCCCGC</p>